

CLAIM

1. A method of altering fibre initiation and/or elongation in a fibre producing plant comprising manipulating said plant such that the production of a polypeptide is
5 modified when compared to a wild-type plant, wherein the polypeptide is a transcription factor, regulatory protein, or a cell cycle protein, produced in said wild type plant at, or around, anthesis.
2. The method of claim 1, wherein the polypeptide comprises a sequence selected
10 from the group consisting of:
 - i) an amino acid sequence provided as any one of SEQ ID NO's:1 to 3 or 12; or
 - ii) an amino acid sequence which is at least 50% identical to any one of SEQ ID NO's:1 to 3 or 12.
- 15 3. The method of claim 2, wherein the polypeptide comprises a sequence selected from the group consisting of:
 - i) an amino acid sequence provided as SEQ ID NO:2; or
 - ii) an amino acid sequence which is at least 80% identical to SEQ ID NO:2.
- 20 4. A method of altering fibre initiation and/or elongation in a fibre producing plant comprising manipulating said plant such that the production of a polypeptide is modified when compared to a wild-type plant, wherein the polypeptide comprises a sequence selected from the group consisting of:
 - i) an amino acid sequence provided as any one of SEQ ID NO's:1 to 16; or
 - 25 ii) an amino acid sequence which is at least 50% identical to any one of SEQ ID NO's:1 to 16.
5. The method of claim 4, wherein the polypeptide comprises a sequence selected from the group consisting of:
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 - i) an amino acid sequence provided as SEQ ID NO:1; or
 - ii) an amino acid sequence which is at least 80% identical to SEQ ID NO:1.
6. The method of claim 4, wherein the polypeptide comprises a sequence selected from the group consisting of:
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 - i) an amino acid sequence provided as SEQ ID NO:2; or
 - ii) an amino acid sequence which is at least 80% identical to SEQ ID NO:2.

7. The method of claim 4, wherein the polypeptide comprises a sequence selected from the group consisting of:
- i) an amino acid sequence provided as SEQ ID NO:3; or
 - 5 ii) an amino acid sequence which is at least 80% identical to SEQ ID NO:3.
8. The method of claim 4, wherein the polypeptide comprises a sequence selected from the group consisting of:
- i) an amino acid sequence provided as SEQ ID NO:12; or
 - 10 ii) an amino acid sequence which is at least 80% identical to SEQ ID NO:12.
9. The method according to any one of claims 1 to 8 which comprises recombinantly expressing the polypeptide in said plant.
- 15 10. The method according to any one of claims 1 to 8 which comprises reducing the level of the polypeptide endogenously produced by the plant.
11. The method of claim 10, wherein the level of the polypeptide endogenously produced by the plant is reduced by exposing the plant to an antisense polynucleotide
- 20 or a catalytic polynucleotide which hybridizes to an mRNA molecule encoding the polypeptide.
12. The method of claim 10, wherein the level of the polypeptide endogenously produced by the plant is reduced by exposing the plant to a dsRNA molecule that
- 25 specifically down-regulates mRNA levels in a cell of an mRNA molecule encoding the polypeptide.
13. The method according to any one of claims 1 to 12, wherein the plant is a horticultural plant.
- 30 14. The method according to any one of claims 1 to 13, wherein the plant is a species of the Genus *Gossypium*.
15. A method of assessing the potential of a fibre producing plant to produce fibre,
- 35 the method comprising analysing the plant for a genetic variation in a polynucleotide associated with fibre initiation and/or elongation, wherein the polynucleotide encodes a

transcription factor, regulatory protein, or a cell cycle protein, produced in a wild type plant at, or around, anthesis

16. The method of claim 15, wherein the polynucleotide comprises a sequence
5 selected from the group consisting of:
- i) a nucleotide sequence provided as any one of SEQ ID NO's:17 to 22, or 38; or
 - ii) a nucleotide sequence which is at least 50% identical to any one of SEQ ID NO's:17 to 22, or 38.
- 10 17. A method of assessing the potential of a fibre producing plant to produce fibre, the method comprising analysing the plant for a genetic variation in a polynucleotide associated with fibre initiation and/or elongation, wherein the polynucleotide comprises a sequence selected from the group consisting of:
- i) a nucleotide sequence provided as any one of SEQ ID NO's:17 to 45; or
 - 15 ii) a nucleotide sequence which is at least 50% identical to any one of SEQ ID NO's:17 to 45.
18. The method according to any one of claims 15 to 17 which comprises performing an amplification reaction on nucleic acids obtained from said plant, or
20 nucleic acids synthesized using nucleic acids from said plant as a template, wherein the production of an amplicon in said amplification reaction indicates an association with fibre producing potential.
19. The method according to any one of claims 15 to 17 which comprises
25 performing an amplification reaction on nucleic acids obtained from said plant, or nucleic acids synthesized using nucleic acids from said plant as a template, wherein the lack of production of an amplicon in said amplification reaction indicates an association with fibre producing potential.
- 30 20. The method according to any one of claims 15 to 17 which comprises performing a hybridization reaction on nucleic acids obtained from said plant, or nucleic acids synthesized using nucleic acids from said plant as a template, wherein a detectable signal produced by the hybridization reaction indicates reduced fibre producing potential.

21. The method according to any one of claims 15 to 17 which comprises performing a hybridization reaction on nucleic acids obtained from said plant, or nucleic acids synthesized using nucleic acids from said plant as a template, wherein the lack of a detectable signal by the hybridization reaction indicates reduced fibre
5 producing potential.

22. The method according to any one of claims 15 to 17, wherein the polynucleotide is mRNA and the method comprises determining the levels of mRNA of the polynucleotide in the plant ovule at, or around, anthesis.

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23. A method of assessing the potential of a fibre producing plant to produce fibre, the method comprising analysing the plant for a polypeptide involved in fibre initiation and/or elongation, wherein the polypeptide is a transcription factor, regulatory protein, or a cell cycle protein, produced in a wild type plant at, or around, anthesis.

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24. A method of assessing the potential of a fibre producing plant to produce fibre, the method comprising analysing the plant for a polypeptide involved in fibre initiation and/or elongation, wherein the polypeptide comprises a sequence selected from the group consisting of:

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- i) an amino acid sequence provided as any one of SEQ ID NO's:1 to 16; or
- ii) an amino acid sequence which is at least 50% identical to any one of SEQ ID NO's:1 to 16.

25. The method of claim 23 or claim 24, wherein the method comprises determining
25 the levels of the polypeptide in the plant ovule at, or around, anthesis.

26. A substantially purified polypeptide selected from the group consisting of:

i) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:1,

30 ii) a polypeptide comprising an amino acid sequence which is at least 87% identical to SEQ ID NO:1, and

iii) a biologically active fragment of i) or ii),

wherein the polypeptide regulates fibre initiation and/or elongation.

35 27. The polypeptide of claim 26, wherein the polypeptide comprises an amino acid sequence which is at least 95% identical to SEQ ID NO:1.

28. A substantially purified polypeptide selected from the group consisting of:
i) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:2, and
5 ii) a biologically active fragment of i),
wherein the polypeptide regulates fibre initiation and/or elongation.
29. A substantially purified polypeptide selected from the group consisting of:
i) a polypeptide comprising an amino acid sequence as provided in SEQ ID
10 NO:3,
ii) a polypeptide comprising an amino acid sequence which is at least 54% identical to SEQ ID NO:3, and
iii) a biologically active fragment of i) or ii),
wherein the polypeptide regulates fibre initiation and/or elongation.
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30. A substantially purified polypeptide selected from the group consisting of:
i) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:4,
ii) a polypeptide comprising an amino acid sequence which is at least 55%
20 identical to SEQ ID NO:4, and
iii) a biologically active fragment of i) or ii),
wherein the polypeptide regulates fibre initiation and/or elongation.
31. A substantially purified polypeptide selected from the group consisting of:
25 i) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:5,
ii) a polypeptide comprising an amino acid sequence which is at least 50% identical to SEQ ID NO:5, and
iii) a biologically active fragment of i) or ii),
30 wherein the polypeptide regulates fibre initiation and/or elongation.
32. A substantially purified polypeptide selected from the group consisting of:
i) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:6,
35 ii) a polypeptide comprising an amino acid sequence which is at least 50% identical to SEQ ID NO:6, and

iii) a biologically active fragment of i) or ii),
wherein the polypeptide regulates fibre initiation and/or elongation.

33. A substantially purified polypeptide selected from the group consisting of:
5 i) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:7,
ii) a polypeptide comprising an amino acid sequence which is at least 79% identical to SEQ ID NO:7, and
iii) a biologically active fragment of i) or ii),
10 wherein the polypeptide regulates fibre initiation and/or elongation.

34. A substantially purified polypeptide selected from the group consisting of:
i) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:8,
15 ii) a polypeptide comprising an amino acid sequence which is at least 66% identical to SEQ ID NO:8, and
iii) a biologically active fragment of i) or ii),
wherein the polypeptide regulates fibre initiation and/or elongation.

- 20 35. A substantially purified polypeptide selected from the group consisting of:
i) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:9,
ii) a polypeptide comprising an amino acid sequence which is at least 95% identical to SEQ ID NO:9, and
25 iii) a biologically active fragment of i) or ii),
wherein the polypeptide regulates fibre initiation and/or elongation.

36. A substantially purified polypeptide selected from the group consisting of:
i) a polypeptide comprising an amino acid sequence as provided in SEQ ID
30 NO:10,
ii) a polypeptide comprising an amino acid sequence which is at least 67% identical to SEQ ID NO:10, and
iii) a biologically active fragment of i) or ii),
wherein the polypeptide regulates fibre initiation and/or elongation.

- 35 37. A substantially purified polypeptide selected from the group consisting of:

- i) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:11,
ii) a polypeptide comprising an amino acid sequence which is at least 55% identical to SEQ ID NO:11, and
5 iii) a biologically active fragment of i) or ii),
wherein the polypeptide regulates fibre initiation and/or elongation.
38. A substantially purified polypeptide selected from the group consisting of:
i) a polypeptide comprising an amino acid sequence as provided in SEQ ID
10 NO:12,
ii) a polypeptide comprising an amino acid sequence which is at least 59% identical to SEQ ID NO:12, and
iii) a biologically active fragment of i) or ii),
wherein the polypeptide regulates fibre initiation and/or elongation.
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39. A substantially purified polypeptide selected from the group consisting of:
i) a polypeptide comprising an amino acid sequence as provided in SEQ ID
NO:13,
ii) a polypeptide comprising an amino acid sequence which is at least 77%
20 identical to SEQ ID NO:13, and
iii) a biologically active fragment of i) or ii),
wherein the polypeptide regulates fibre initiation and/or elongation.
40. A substantially purified polypeptide selected from the group consisting of:
25 i) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:14,
ii) a polypeptide comprising an amino acid sequence which is at least 50% identical to SEQ ID NO:14, and
iii) a biologically active fragment of i) or ii),
30 wherein the polypeptide regulates fibre initiation and/or elongation.
41. A substantially purified polypeptide selected from the group consisting of:
i) a polypeptide comprising an amino acid sequence as provided in SEQ ID
NO:15,
35 ii) a polypeptide comprising an amino acid sequence which is at least 64% identical to SEQ ID NO:15, and

iii) a biologically active fragment of i) or ii),
wherein the polypeptide regulates fibre initiation and/or elongation.

42. A substantially purified polypeptide selected from the group consisting of:

5 i) a polypeptide comprising an amino acid sequence as provided in SEQ ID NO:16,

ii) a polypeptide comprising an amino acid sequence which is at least 50% identical to SEQ ID NO:16, and

10 iii) a biologically active fragment of i) or ii),
wherein the polypeptide regulates fibre initiation and/or elongation.

43. The polypeptide according to any one of claims 26 to 42, wherein the polypeptide can be purified from a species of the Genus *Gossypium*.

15 44. The polypeptide according to any one of claims 26 to 43, which is a fusion protein further comprising at least one other polypeptide sequence.

45. An isolated polynucleotide comprising a sequence of nucleotides selected from the group consisting of:

20 i) a sequence of nucleotides as provided in SEQ ID NO:17;

ii) a sequence of nucleotides as provided in SEQ ID NO:18;

iii) a sequence encoding a polypeptide according to claim 19 or claim 20;

iv) a sequence of nucleotides which is at least 87% identical to SEQ ID NO:17 or SEQ ID NO:18; and

25 v) a sequence which hybridizes to any one of i) to iv) under high stringency conditions,

wherein the polynucleotide does not comprise a sequence of nucleotides as provided in SEQ ID NO:46.

30 46. An isolated polynucleotide comprising a sequence of nucleotides selected from the group consisting of:

i) a sequence of nucleotides as provided in SEQ ID NO:19,

ii) a sequence of nucleotides as provided in SEQ ID NO:20,

iii) a sequence encoding a polypeptide according to claim 21, and

35 iv) a sequence complementary to any one of i) to iii).

47. An isolated polynucleotide comprising a sequence of nucleotides selected from the group consisting of:

- i) a sequence of nucleotides as provided in SEQ ID NO:21;
- ii) a sequence of nucleotides as provided in SEQ ID NO:22;
- 5 iii) a sequence encoding a polypeptide according to claim 22;
- iv) a sequence of nucleotides which is at least 54% identical to SEQ ID NO:21 or SEQ ID NO:22; and
- v) a sequence which hybridizes to any one of i) to iv) under high stringency conditions,

10 wherein the polynucleotide does not comprise a sequence of nucleotides as provided in SEQ ID NO:47.

48. An isolated polynucleotide comprising a sequence of nucleotides selected from the group consisting of:

- 15 i) a sequence of nucleotides as provided in SEQ ID NO:23;
- ii) a sequence encoding a polypeptide according to claim 23;
- iii) a sequence of nucleotides which is at least 55% identical to SEQ ID NO:23; and
- iv) a sequence which hybridizes to any one of i) to iii) under high stringency
- 20 conditions,

wherein the polynucleotide does not comprise a sequence of nucleotides as provided in SEQ ID NO:48.

49. An isolated polynucleotide comprising a sequence of nucleotides selected from the group consisting of:

- 25 i) a sequence of nucleotides as provided in SEQ ID NO:24;
- ii) a sequence of nucleotides as provided in SEQ ID NO:25;
- iii) a sequence encoding a polypeptide according to claim 24;
- iv) a sequence of nucleotides which is at least 50% identical to SEQ ID NO:24 or SEQ ID NO:25; and
- 30 v) a sequence which hybridizes to any one of i) to iv) under high stringency conditions,

wherein the polynucleotide does not comprise a sequence of nucleotides as provided in SEQ ID NO:49.

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50. An isolated polynucleotide comprising a sequence of nucleotides selected from the group consisting of:
- i) a sequence of nucleotides as provided in SEQ ID NO:26;
 - ii) a sequence of nucleotides as provided in SEQ ID NO:27;
 - 5 iii) a sequence encoding a polypeptide according to claim 25;
 - iv) a sequence of nucleotides which is at least 50% identical to SEQ ID NO:26 or SEQ ID NO:27; and
 - v) a sequence which hybridizes to any one of i) to iv) under high stringency conditions,
- 10 wherein the polynucleotide does not comprise a sequence of nucleotides as provided in SEQ ID NO:50.
51. An isolated polynucleotide comprising a sequence of nucleotides selected from the group consisting of:
- 15 i) a sequence of nucleotides as provided in SEQ ID NO:28,
 - ii) a sequence of nucleotides as provided in SEQ ID NO:29,
 - iii) a sequence encoding a polypeptide according to claim 26,
 - iv) a sequence complementary to any one of i) to iii).
- 20 52. An isolated polynucleotide comprising a sequence of nucleotides selected from the group consisting of:
- i) a sequence of nucleotides as provided in SEQ ID NO:30;
 - ii) a sequence of nucleotides as provided in SEQ ID NO:31;
 - iii) a sequence encoding a polypeptide according to claim 27;
 - 25 iv) a sequence of nucleotides which is at least 65% identical to SEQ ID NO:30 or SEQ ID NO:31; and
 - v) a sequence which hybridizes to any one of i) to iv) under high stringency conditions,
- wherein the polynucleotide does not comprise a sequence of nucleotides as
- 30 provided in SEQ ID NO:51.
53. An isolated polynucleotide comprising a sequence of nucleotides selected from the group consisting of:
- i) a sequence of nucleotides as provided in SEQ ID NO:32,
 - 35 ii) a sequence of nucleotides as provided in SEQ ID NO:33,
 - iii) a sequence encoding a polypeptide according to claim 28,

iv) a sequence complementary to any one of i) to iii).

54. An isolated polynucleotide comprising a sequence of nucleotides selected from the group consisting of:

- 5 i) a sequence of nucleotides as provided in SEQ ID NO:34;
 ii) a sequence of nucleotides as provided in SEQ ID NO:35;
 iii) a sequence encoding a polypeptide according to claim 29;
 iv) a sequence of nucleotides which is at least 70% identical to SEQ ID NO:34
or SEQ ID NO:35; and
10 v) a sequence which hybridizes to any one of i) to iv) under high stringency
conditions,

wherein the polynucleotide does not comprise a sequence of nucleotides as provided in SEQ ID NO:52.

15 55. An isolated polynucleotide comprising a sequence of nucleotides selected from the group consisting of:

- i) a sequence of nucleotides as provided in SEQ ID NO:36;
 ii) a sequence of nucleotides as provided in SEQ ID NO:37;
 iii) a sequence encoding a polypeptide according to claim 30;
20 iv) a sequence of nucleotides which is at least 55% identical to SEQ ID NO:36
or SEQ ID NO:37; and
 v) a sequence which hybridizes to any one of i) to iv) under high stringency
conditions,

wherein the polynucleotide does not comprise a sequence of nucleotides as
25 provided in SEQ ID NO:53.

56. An isolated polynucleotide comprising a sequence of nucleotides selected from the group consisting of:

- i) a sequence of nucleotides as provided in SEQ ID NO:38;
30 ii) a sequence encoding a polypeptide according to claim 31;
 iii) a sequence of nucleotides which is at least 65% identical to SEQ ID NO:38;
and
 iv) a sequence which hybridizes to any one of i) to iii) under high stringency
conditions.

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57. An isolated polynucleotide comprising a sequence of nucleotides selected from the group consisting of:
- i) a sequence of nucleotides as provided in SEQ ID NO:39;
 - ii) a sequence of nucleotides as provided in SEQ ID NO:40;
 - 5 iii) a sequence encoding a polypeptide according to claim 32;
 - iv) a sequence of nucleotides which is at least 95% identical to SEQ ID NO:39 or SEQ ID NO:40; and
 - v) a sequence which hybridizes to any one of i) to iv) under high stringency conditions,
- 10 wherein the polynucleotide does not comprise a sequence of nucleotides as provided in SEQ ID NO:54.
58. An isolated polynucleotide comprising a sequence of nucleotides selected from the group consisting of:
- 15 i) a sequence of nucleotides as provided in SEQ ID NO:41;
 - ii) a sequence of nucleotides as provided in SEQ ID NO:42;
 - iii) a sequence encoding a polypeptide according to claim 33;
 - iv) a sequence of nucleotides which is at least 50% identical to SEQ ID NO:41 or SEQ ID NO:42; and
 - 20 v) a sequence which hybridizes to any one of i) to iv) under high stringency conditions,
- wherein the polynucleotide does not comprise a sequence of nucleotides as provided in SEQ ID NO:55.
- 25 59. An isolated polynucleotide comprising a sequence of nucleotides selected from the group consisting of:
- i) a sequence of nucleotides as provided in SEQ ID NO:43;
 - ii) a sequence of nucleotides as provided in SEQ ID NO:44;
 - iii) a sequence encoding a polypeptide according to claim 34;
 - 30 iv) a sequence of nucleotides which is at least 65% identical to SEQ ID NO:43 or SEQ ID NO:44; and
 - v) a sequence which hybridizes to any one of i) to iv) under high stringency conditions,
- wherein the polynucleotide does not comprise a sequence of nucleotides as
35 provided in SEQ ID NO:56.

60. An isolated polynucleotide comprising a sequence of nucleotides selected from the group consisting of:
- i) a sequence of nucleotides as provided in SEQ ID NO:45;
 - ii) a sequence encoding a polypeptide according to claim 35;
 - 5 iii) a sequence of nucleotides which is at least 50% identical to SEQ ID NO:45;
- and
- iv) a sequence which hybridizes to any one of i) to iii) under high stringency conditions,
- wherein the polynucleotide does not comprise a sequence of nucleotides as
- 10 provided in SEQ ID NO:57.
61. A catalytic polynucleotide capable of cleaving a polynucleotide according to any one of claims 45 to 60.
- 15 62. The catalytic polynucleotide of claim 61 which is a ribozyme.
63. An oligonucleotide which comprises at least 19 contiguous nucleotides of a polynucleotide according to any one of claims 45 to 60.
- 20 64. A double stranded RNA (dsRNA) molecule comprising an oligonucleotide according to claim 63, wherein the portion of the molecule that is double stranded is at least 19 basepairs in length and comprises said oligonucleotide.
65. The dsRNA molecule of claim 64 which is expressed from a single promoter,
- 25 wherein the strands of the double stranded portion are linked by a single stranded portion.
66. A vector comprising or encoding the polynucleotide according to any one of claims 45 to 60.
- 30 67. The vector of claim 66 wherein the polynucleotide is operably linked to an ovule or fibre specific promoter.
68. A vector comprising or encoding oligonucleotide of claim 63 or the dsRNA
- 35 molecule of claim 64.

69. A host cell comprising the vector according to any one of claims 66 to 68.

70. A transgenic plant, the plant having been transformed with polynucleotide according to any one of claims 45 to 60 or the oligonucleotide of claim 63.

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71. The transgenic plant of claim 70 wherein the polynucleotide is capable of expression to produce a polypeptide according to any one of claims 26 to 44.

72. A transgenic plant, the plant having been transformed such that it produces a catalytic polynucleotide of claim 61 or claim 62, or a dsRNA molecule of claim 64 or claim 65.

73. The transgenic plant of claim 70 or claim 72, wherein the polynucleotide, catalytic polynucleotide or dsRNA down-regulates the production of a polypeptide according to any one of claims 26 to 44 which is endogenously produced by the plant.

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74. A substantially purified antibody, or fragment thereof, that specifically binds a polypeptide according to any one of claims 26 to 44.

75. A method of breeding a fibre producing plant, the method comprising performing a method according to any one of claims 15 to 25.

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76. A method of selecting from a breeding population a fibre producing plant with altered fibre initiation and/or elongation potential, the method comprising;

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i) crossing two plants which have differing potential to produce fibre,

ii) performing a method according to any one of claims 15 to 25 on progeny plants,

iii) selecting a progeny plant with altered fibre initiation and/or elongation potential when compared to a parent plant.

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77. A plant produced by the method of claim 75 or claim 76.

78. Seed of a plant of any one of claims 70 to 73 or claim 77.

79. Fibre of a plant of any one of claims 70 to 73 or claim 77.

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80. A method of identifying an agent which alters fibre initiation and/or elongation of a fibre producing plant, the method comprising

a) exposing a polypeptide which is at least 50% identical to any one of SEQ ID NO's:1 to 16 to a candidate agent, and

5 b) assessing the ability of the candidate agent to modulate the activity of the polypeptide.

81. A method of identifying an agent which alters fibre initiation and/or elongation of a fibre producing plant, the method comprising

10 a) exposing a polypeptide which is at least 50% identical to any one of SEQ ID NO's:1 to 16 to a binding partner which binds the polypeptide, and a candidate agent, and

b) assessing the ability of the candidate agent to compete with the binding partner for binding to the polypeptide.

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82. The method of claim 81, wherein the binding partner is detectably labeled.

83. A method of identifying an agent which alters fibre initiation and/or elongation of a fibre producing plant, the method comprising

20 a) exposing a polynucleotide encoding a polypeptide which is at least 50% identical to any one of SEQ ID NO's:1 to 16 to a candidate agent under conditions which allow expression of the polynucleotide, and

b) assessing the ability of the candidate agent to modulate levels of polypeptide produced by the polynucleotide.

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84. A method of identifying an agent which alters fibre initiation and/or elongation of a fibre producing plant, the method comprising

a) exposing a polynucleotide which is at least 50% identical to any one of SEQ ID NO's:17 to 45 to a candidate agent, and

30 b) assessing the ability of the candidate agent to hybridize and/or cleave the polynucleotide.